<110>

```
Heston, Warren D.W.
               O'Keefe, Denise S.
     <120>
               DNA Encoding the Prostate-Specific Membrane
               Antigen-Like Gene and Uses Thereof
     <130>
               D6230
     <141>
               2001-10-09
     <150>
               PCT/US00/09417
     <151>
               2000-04-09
     <160>
               38
     <210>
     <211>
               1992
     <212>
               DNA
     <213>
               Homo sapiens
     <223>
               cDNA sequence of PSMA-like gene
     <400>
               1
                                                          50
agcaaatact cactaccaca aataagaaca tttccaaatc tgatgttctg
                                                        100
aggattttta gagcttatag tagcaaaaag aaaagggaaa ttctctctga
                                                        150
gatgtccttt tttgtaggcc taatgacaaa aggttgaaga taaagttcta
                                                        200
qtactcattt aagtgtaata ttgaaaattg atattaccaa atctggaaca
accaatttaa aataaggaaa gaaagacact gtgttttcta ggttaaaaaat
                                                        250
gcccagctgg caggggccaa aggagtcatt ctctactcag accctgctga
                                                        300
ctactttgct cctggggtga agtcctatcc agacggttgg aatcttcctg
                                                        350
                                                        400
qaqqtqqtqt ccaqcqtqqa aatatcctaa atctgaatgg tgcaggagac
                                                        450
cctctcacac caggttaccc agcaaatgaa tacgcttata ggcatggaat
tgcagaggct gttggtcttc caagtattcc tgttcatcca gttggatact
                                                         500
atgatgcaca gaagctccta gaaaaaatgg gtggctcagc accaccagat
                                                         550
ageagetgga gaggaagtet caaagtgtee tacaatgttg gacetggett
                                                        600
                                                        650
tactggaaac ttttctacac aaaaagtcaa gatgcacatc cactctacca
atgaagtgac gagaatttac aatgtgatag gtactctcag aggagcagtg
                                                        700
                                                        750
gaaccagaca gatatgtcat tctgggaggt caccgggact catgggtgtt
tggtggtatt gaccctcaga gtggagcagc tgttgttcat gaaactgtga
                                                        800
ggagctttgg aacactgaaa aaggaagggt ggagacctag aagaacaatt
                                                        850
ttgtttgcaa gctgggatgc agaagaattt ggtcttcttg gttctactga
                                                        900
qtqqqcaqaq qataattcaa gactccttca agagcgtggc gtggcttata
ttaatqctqa ctcatctata gaaggaaact acactctgag agttgattgt 1000
acaccactga tgtacagctt ggtatacaac ctaacaaaag agctgaaaag 1050
ccctgatgaa ggctttgaag gcaaatctct ttatgaaagt tggactaaaa 1100
aaagtccttc cccagagttc agtggcatgc ccaggataag caaattggga 1150
tctggaaatg attttgaggt gttcttccaa cgacttggaa ttgcttcagg 1200
cagagcacgg tatactaaaa attgggaaac aaacaaattc agcggctatc 1250
cactgtatca cagtgtctat gaaacatatg agttggtgga aaagttttat 1300
gatccaatgt ttaaatatca cctcactgtg gcccaggttc gaggagggat 1350
ggtgtttgag ctagccaatt ccatagtgct cccttttgat tgtcgagatt 1400
atgctgtagt tttaagaaag tatgctgaca aaatctacaa tatttctatg 1450
```

```
aaacatccac aggaaatgaa gacatacagt ttatcatttg attcactttt 1500
ttctgcagta aaaaatttta cagaaattgc ttccaagttc agcgagagac 1550
tccaggactt tgacaaaagc aacccaatat tgttaagaat gatgaatgat 1600
caactcatgt ttctggaaag agcatttatt gatccattag ggttaccaga 1650
cagacetttt tataggeatg teatetatge tecaageage caeaacaagt 1700
atgcagggga gtcattccca ggaatttatg atgctctgtt tgatattgaa 1750
agcaaaqtqq accettccaa qqcetqqqqa qatqtqaaqa qacagatttc 1800
tgttgcagcc ttcacagtgc aggcagctgc agagactttg agtgaagtag 1850
cctaagagga ttctttagag actctgtatt gaatttgtgt ggtatgtcac 1900
tcaaagaata ataatgggta tattgataaa ttttaaaatt ggtatatttg 1950
1992
     <210>
               2
               442
     <211>
     <212>
               PRT
     <213>
               Homo sapiens
     <220>
               deduced amino acid sequence of PSMA-like
     <223>
               protein
     <400>
Met Gly Gly Ser Ala Pro Pro Asp Ser Ser Trp Arg Gly Ser Leu
                                    10
                                                        15
Lys Val Ser Tyr Asn Val Gly Pro Gly Phe Thr Gly Asn Phe Ser
                20
                                    25
                                                        30
Thr Gln Lys Val Lys Met His Ile His Ser Thr Asn Glu Val Thr
                35
                                    40
                                                        45
Arg Ile Tyr Asn Val Ile Gly Thr Leu Arg Gly Ala Val Glu Pro
                                    55
Asp Arg Tyr Val Ile Leu Gly Gly His Arg Asp Ser Trp Val Phe
                65
                                    70
                                                        75
Gly Gly Ile Asp Pro Gln Ser Gly Ala Ala Val Val His Glu Thr
                80
                                    85
                                                        90
Val Arg Ser Phe Gly Thr Leu Lys Lys Glu Gly Trp Arg Pro Arg
                95
                                    100
Arg Thr Ile Leu Phe Ala Ser Trp Asp Ala Glu Glu Phe Gly Leu
                110
                                    115
                                                        120
Leu Gly Ser Thr Glu Trp Ala Glu Asp Asn Ser Arg Leu Leu Gln
                125
                                    130
                                                        135
Glu Arg Gly Val Ala Tyr Ile Asn Ala Asp Ser Ser Ile Glu Gly
                140
                                    145
                                                        150
```

Asn	Tyr	Thr	Leu	Arg	Val	Asp	Cys	Thr	Pro 160	Leu	Met	Tyr	Ser	Leu 165
7727	Пъ тъ	7 an	Lou		Larc	Glu	Len	Luc		Dro	λen	Glu	Gly	
vai	ıyı	ASII	пеа	170	цуз	GIU	цец	цур	175	110	dan	Giu	GIY	180
Glu	Glaz	Larc	Sor		Туг	Glu	Ser	Ψ×τ.		Tare	Tare	Ser	Pro	
Giu	GIY	БУБ	Ser	185	ıyı	Giu	Der	пр	190	БУБ	пур	Der	110	195
Dro	Glu	Dho	Ser		Met	Pro	Δra	Tle		Lve	T.e.u	Glv	Ser	
110	Olu	1110	DCI	200	1100	110	111.9	110	205	טענב	Lea	O _T	DCI	210
Asn	Asp	Phe	Glu		Phe	Phe	Gln	Ara		Glv	Tle	Ala	Ser	
11011	1105	1110	OLG	215	1110	11.0	0111	9	220	0-1			501	225
Ara	Ala	Ara	Tvr		Lvs	Asn	Trp	Glu		Asn	Lvs	Phe	Ser	
9		5	-1 -	230	-1 -				235					240
Tyr	Pro	Leu	Tyr		Ser	Val	Tyr	Glu		Tyr	Glu	Leu	Val	
-			_	245			_		250					255
Lys	Phe	Tyr	Asp	Pro	Met	Phe	Lys	Tyr	His	Leu	Thr	Val	Ala	Gln
				260					265					270
Val	Arg	Gly	Gly	Met	Val	Phe	Glu	Leu	Ala	Asn	Ser	Ile	Val	Leu
				275					280					285
Pro	Phe	Asp	Cys	Arg	Asp	Tyr	Ala	Val	Val	Leu	Arg	Lys	Tyr	Ala
				290					295					300
Asp	Lys	Ile	Tyr	Asn	Ile	Ser	Met	Lys	His	Pro	Gln	Glu	Met	Lys
				305					310					315
Thr	Tyr	Ser	Leu	Ser	Phe	Asp	Ser	Leu	Phe	Ser	Ala	Val	Lys	Asn
				320					325					330
Phe	Thr	Glu	Ile	Ala	Ser	Lys	Phe	Ser	Glu	Arg	Leu	Gln	Asp	Phe
				335					340					345
Asp	Lys	Ser	Asn		Ile	Leu	Leu	Arg		Met	Asn	Asp	Gln	
				350					355		_			360
Met	Phe	Leu	Glu	_	Ala	Phe	Ile	Asp		Leu	Gly	Leu	Pro	
		_		365		_	_		370				•	375
Arg	Pro	Phe	Tyr	_	His	Val	Ile	Tyr		Pro	Ser	Ser	His	
_	_		~7	380	~	-1	_	~ 3	385	-	_	~ 7	_	390
ГЛЗ	Tyr	Ala	GIY		Ser	Phe	Pro	GIY		Tyr	Asp	Ala	Leu	
				395					400					405

```
Asp Ile Glu Ser Lys Val Asp Pro Ser Lys Ala Trp Gly Asp Val
                                                         420
                410
                                    415
Lys Arg Gln Ile Ser Val Ala Ala Phe Thr Val Gln Ala Ala Ala
                425
                                    430
                                                         435
Glu Thr Leu Ser Glu Val Ala
                440
     <210>
               2653
     <211>
               DNA
     <212>
     <213>
               Homo sapiens
     <220>
     <223>
               nucleotide sequence of human PSMA gene
     <300>
               GenBank Accession No. M99487
     <308>
     <400>
                                                          50
ctcaaaaqqq gccggatttc cttctcctgg aggcagatgt tgcctctctc
                                                         100
tctcgctcgg attggttcag tgcactctag aaacactgct gtggtggaga
                                                         150
aactqqaccc caggtctgga gcgaattcca gcctgcaggg ctgataagcg
aggcattagt gagattgaga gagactttac cccgccgtgg tggttggagg
                                                         200
gcgcgcagta gagcagcagc acaggcgcgg gtcccgggag gccggctctg
                                                         250
ctcgcgccga gatgtggaat ctccttcacg aaaccgactc ggctgtggcc
                                                         300
accgcgcgcc gcccgcgctg gctgtgcgct ggggcgctgg tgctggcggg
                                                         350
tggcttcttt ctcctcggct tcctcttcgg gtggtttata aaatcctcca
                                                         400
atgaagctac taacattact ccaaagcata atatgaaagc atttttggat
                                                         450
gaattgaaag ctgagaacat caagaagttc ttatataatt ttacacagat
                                                         500
accacattta gcaggaacag aacaaaactt tcagcttgca aagcaaattc
                                                         550
aatcccagtg gaaagaattt ggcctggatt ctgttgagct agcacattat
                                                         600
gatgtcctgt tgtcctaccc aaataagact catcccaact acatctcaat
                                                         650
                                                         700
aattaatgaa gatggaaatg agattttcaa cacatcatta tttgaaccac
ctcctccagg atatgaaaat gtttcggata ttgtaccacc tttcagtgct
                                                         750
ttctctcctc aaggaatgcc agagggcgat ctagtgtatg ttaactatgc
                                                         800
                                                         850
acgaactgaa gacttcttta aattggaacg ggacatgaaa atcaattgct
ctgggaaaat tgtaattgcc agatatggga aagttttcag aggaaataag
                                                         900
gttaaaaatg cccagctggc aggggccaaa ggagtcattc tctactccga
ccctgctgac tactttgctc ctggggtgaa gtcctatcca gatggttgga 1000
atcttcctgg aggtggtgtc cagcgtggaa atatcctaaa tctgaatggt 1050
gcaggagacc ctctcacacc aggttaccca gcaaatgaat atgcttatag 1100
gcgtggaatt gcagaggctg ttggtcttcc aagtattcct gttcatccaa 1150
ttggatacta tgatgcacag aagctcctag aaaaaatggg tggctcagca 1200
ccaccagata gcagctggag aggaagtctc aaagtgccct acaatgttgg 1250
acctggcttt actggaaact tttctacaca aaaagtcaag atgcacatcc 1300
actctaccaa tgaagtgaca agaatttaca atgtgatagg tactctcaga 1350
ggagcagtgg aaccagacag atatgtcatt ctgggaggtc accgggactc 1400
atgggtgttt ggtggtattg accctcagag tggagcagct gttgttcatg 1450
```

```
aaattqtqaq qaqctttqqa acactgaaaa aggaagggtg gagacctaqa 1500
agaacaattt tgtttgcaag ctgggatgca gaagaatttg gtcttcttgg 1550
ttctactgag tgggcagagg agaattcaag actccttcaa gagcgtggcg 1600
tggcttatat taatgctgac tcatctatag aaggaaacta cactctgaga 1650
qttqattqta caccgctgat gtacagcttg gtacacaacc taacaaaaga 1700
gctgaaaagc cctgatgaag gctttgaagg caaatctctt tatgaaagtt 1750
ggactaaaaa aagteettee eeagagttea gtggcatgee caggataage 1800
aaattgggat ctggaaatga ttttgaggtg ttcttccaac gacttggaat 1850
tgcttcaggc agagcacggt atactaaaaa ttgggaaaca aacaaattca 1900
geggetatee aetgtateae agtgtetatg aaacatatga gttggtggaa 1950
aagttttatg atccaatgtt taaatatcac ctcactgtgg cccaggttcg 2000
aggagggatg gtgtttgagc tagccaattc catagtgctc ccttttgatt 2050
qtcqaqatta tgctgtagtt ttaagaaagt atgctgacaa aatctacagt 2100
atttctatga aacatccaca ggaaatgaag acatacagtg tatcatttga 2150
ttcacttttt tctgcagtaa agaattttac agaaattgct tccaagttca 2200
gtgagagact ccaggacttt gacaaaagca acccaatagt attaagaatg 2250
atgaatgatc aactcatgtt tctggaaaga gcatttattg atccattagg 2300
gttaccagac aggeettttt ataggeatgt catetatget ccaagcagec 2350
acaacaagta tgcaggggag tcattcccag gaatttatga tgctctgttt 2400
gatattgaaa gcaaagtgga cccttccaag gcctggggag aagtgaagag 2450
acagatttat gttgcagcct tcacagtgca ggcagctgca gagactttga 2500
gtgaagtagc ctaagaggat tctttagaga atccgtattg aatttgtgtg 2550
gtatgtcact cagaaagaat cgtaatgggt atattgataa attttaaaat 2600
2653
aaa
     <210>
     <211>
               750
     <212>
               PRT
     <213>
               Homo sapiens
     <220>
     <223>
               deduced amino acid sequence of PSMA protein
     <400>
Met Trp Asn Leu Leu His Glu Thr Asp Ser Ala Val Ala Thr Ala
                5
                                   10
                                                       15
Arg Arg Pro Arg Trp Leu Cys Ala Gly Ala Leu Val Leu Ala Gly
                                                       30
                                   25
Gly Phe Phe Leu Leu Gly Phe Leu Phe Gly Trp Phe Ile Lys Ser
                                   40
                                                       45
                35
Ser Asn Glu Ala Thr Asn Ile Thr Pro Lys His Asn Met Lys Ala
                                                       60
                50
                                   55
Phe Leu Asp Glu Leu Lys Ala Glu Asn Ile Lys Lys Phe Leu Tyr
```

65

70

75

Asn	Phe	Thr	Gln	Ile 80	Pro	His	Leu	Ala	Gly 85	Thr	Glu	Gln	Asn	Phe 90
Gln	Leu	Ala	Lys	Gln 95	Ile	Gln	Ser	Gln	Trp 100	Lys	Glu	Phe	Gly	Leu 105
Asp	Ser	Val	Glu	Leu 110	Ala	His	Tyr	Asp	Val 115	Leu	Leu	Ser	Tyr	Pro 120
Asn	Lys	Thr	His	Pro 125	Asn	Tyr	Ile	Ser	Ile 130	Ile	Asn	Glu	Asp	Gly 135
Asn	Glu	Ile	Phe	Asn 140	Thr	Ser	Leu	Phe	Glu 145	Pro	Pro	Pro	Pro	Gly 150
Tyr	Glu	Asn	Val	Ser 155	Asp	Ile	Val	Pro	Pro 160	Phe	Ser	Ala	Phe	Ser 165
Pro	Gln	Gly	Met	Pro 170	Glu	Gly	Asp	Leu	Val 175	Tyr	Val	Asn	Tyr	Ala 180
Arg	Thr	Glu	Asp	Phe 185	Phe	Lys	Leu	Glu	Arg 190	Asp	Met	Lys	Ile	Asn 195
Cys	Ser	Gly	Lys	Ile 200	Val	Ile	Ala	Arg	Tyr 205	Gly	Lys	Val	Phe	Arg 210
Gly	Asn	Lys	Val	Lys 215	Asn	Ala	Gln	Leu	Ala 220	Gly	Ala	Lys	Gly	Val 225
Ile	Leu	Tyr	Ser	Asp 230	Pro	Ala	Asp	Tyr	Phe 235	Ala	Pro	Gly	Val	Lys 240
Ser	Tyr	Pro	Asp	Gly 245	Trp	Asn	Leu	Pro	Gly 250	Gly	Gly	Val	Gln	Arg 255
Gly	Asn	Ile	Leu	Asn 260	Leu	Asn	Gly	Ala	Gly 265	Asp	Pro	Leu	Thr	Pro 270
Gly	Tyr	Pro	Ala	Asn 275	Glu	Tyr	Ala	Tyr	Arg 280	Arg	Gly	Ile	Ala	Glu 285
Ala	Val	Gly	Leu	Pro 290	Ser	Ile	Pro	Val	His 295	Pro	Ile	Gly	Tyr	Tyr 300
Asp	Ala	Gln	Lys	Leu 305	Leu	Glu	Lys	Met	Gly 310	Gly	Ser	Ala	Pro	Pro 315
Asp	Ser	Ser	Trp	Arg 320	Gly	Ser	Leu	Lys	Val 325	Pro	Tyr	Asn	Val	Gly 330

Pro	Gly	Phe	Thr	Gly 335	Asn	Phe	Ser	Thr	Gln 340	Lys	Val	Lys	Met	His
Ile	His	Ser	Thr	Asn	Glu	Val	Thr	Arg	Ile	Tyr	Asn	Val	Ile	Gly
				350					355					360
Thr	Leu	Arg	Gly	Ala 365	Val	Glu	Pro	Asp	Arg 370	Tyr	Val	Ile	Leu	Gly 375
Gly	His	Arg	Asp	Ser	Trp	Val	Phe	Gly	Gly	Ile	Asp	Pro	Gln	Ser
				380					385					390
Gly	Ala	Ala	Val	Val	His	Glu	Ile	Val	Arg	Ser	Phe	Gly	Thr	Leu
				395					400					405
Lys	Lys	Glu	Gly	Trp	Arg	Pro	Arg	Arg	Thr	Ile	Leu	Phe	Ala	Ser
				410					415					420
Trp	Asp	Ala	Glu	Glu	Phe	Gly	Leu	Leu	Gly	Ser	Thr	Glu	Trp	Ala
				425					430					435
Glu	Glu	Asn	Ser	Arg	Leu	Leu	Gln	Glu	Arg	Gly	Val	Ala	Tyr	Ile
				440					445					450
Asn	Ala	Asp	Ser	Ser	Ile	Glu	Gly	Asn	Tyr	Thr	Leu	Arg	Val	Asp
				455					460					465
Cys	Thr	Pro	Leu	Met	Tyr	Ser	Leu	Val	His	Asn	Leu	Thr	Lys	Glu
				470					475					480
Leu	Lys	Ser	Pro	Asp	Glu	Gly	Phe	Glu	Gly	Lys	Ser	Leu	Tyr	Glu
				485					490					495
Ser	Trp	Thr	Lys	Lys	Ser	Pro	Ser	Pro	Glu	Phe	Ser	Gly	Met	Pro
				500					505					510
Arg	Ile	Ser	Lys	Leu	Gly	Ser	Gly	Asn	Asp	Phe	Glu	Val	Phe	Phe
				515					520					525
Gln	Arg	Leu	Gly	Ile	Ala	Ser	Gly	Arg	Ala	Arg	Tyr	Thr	Lys	Asn
				530					535					540
Trp	Glu	Thr	Asn	Lys	Phe	Ser	Gly	Tyr	Pro	Leu	Tyr	His	Ser	Val
				545					550					555
Tyr	Glu	Thr	Tyr	Glu	Leu	Val	Glu	Lys	Phe	Tyr	Asp	Pro	Met	Phe
				560					565					570
Lys	Tyr	His	Leu	Thr	Val	Ala	Gln	Val	Arg	Gly	Gly	Met	Val	Phe
				575					580					585

```
Glu Leu Ala Asn Ser Ile Val Leu Pro Phe Asp Cys Arg Asp Tyr
                                      595
                                                          600
                 590
Ala Val Val Leu Arg Lys Tyr Ala Asp Lys Ile Tyr Ser Ile Ser
                 605
                                      610
                                                          615
Met Lys His Pro Gln Glu Met Lys Thr Tyr Ser Val Ser Phe Asp
                 620
                                      625
                                                          630
Ser Leu Phe Ser Ala Val Lys Asn Phe Thr Glu Ile Ala Ser Lys
                 635
                                     640
Phe Ser Glu Arg Leu Gln Asp Phe Asp Lys Ser Asn Pro Ile Val
                                      655
                                                          660
                 650
Leu Arg Met Met Asn Asp Gln Leu Met Phe Leu Glu Arg Ala Phe
                                      670
                 665
Ile Asp Pro Leu Gly Leu Pro Asp Arg Pro Phe Tyr Arg His Val
                 680
                                      685
Ile Tyr Ala Pro Ser Ser His Asn Lys Tyr Ala Gly Glu Ser Phe
                                      700
                                                          705
                 695
Pro Gly Ile Tyr Asp Ala Leu Phe Asp Ile Glu Ser Lys Val Asp
                 710
                                     715
                                                          720
Pro Ser Lys Ala Trp Gly Glu Val Lys Arg Gln Ile Tyr Val Ala
                                      730
                 725
                                                          735
Ala Phe Thr Val Gln Ala Ala Glu Thr Leu Ser Glu Val Ala
                                     745
                                                          750
                 740
                5
     <210>
     <211>
                28
     <212>
                DNA
     <213>
                Artificial sequence
     <220>
     <221>
                primer_bind
                sense primer designed for only amplifying
     <223>
                the first intron of the PSMA-like gene on
                chromosome 11q
     <400>
                                                   28
gccttcattt tcagaacatc tcatgcat
     <210>
                6
     <211>
                25
```

<212> <213>		
<220> <221> <223>	primer_bind	intron of the PSMA-
<400>	6	
gtccatataa	actttcaaga atgtg	25
J	• • •	
<210> <211> <212> <213>	20 DNA	
<220> <221> <223>	primer_bind	f the PSMA genomic y the corresponding
<400>	7	
	gtcagaggta	20
000000000	5000303500	
<210> <211> <212> <213>	20 DNA Artificial sequence	
<221> <223>		y the corresponding
<400>	8	
agtatagtcc		
	tcctcagatg	20
<210> <211> <212> <213>	9 24 DNA	20
<211> <212>	9 24 DNA	20

<223>	sense oligonucleotide primer based upon intronic sequences of the PSMA genomic clone used to amplify the corresponding regions of the PSMA-like gene (exon 3)
<400> caaagtactt	9 ttgtgtaact ctgc 24
<210> <211> <212> <213>	22 DNA
<220> <221> <223>	primer_bind
<400>	10
cataggaaag	tagttgacac gg 22
<210> <211> <212> <213>	22 DNA Artificial sequence
<220> <221> <223>	primer_bind
<400>	
cctgaaggat	tcattcaccc tc 22
<210> <211> <212> <213>	DNA
<220> <221> <223>	primer_bind antisense oligonucleotide primer based upon intronic sequences of the PSMA genomic clone used to amplify the corresponding regions of the PSMA-like gene (exon 4)

<210> <211> <212> <213>	22 DNA
<220> <221> <223>	primer_bind
<400>	16
ttacccaaat	agccatccat gg 22
<210> <211> <212> <213>	23 DNA
<220> <221> <223>	primer_bind
<400>	17
gcagatgctc	aataagtgaa tcc 23
<210> <211> <212> <213>	24 DNA
<220> <221> <223>	<u>-</u>
<400> ccagcacata	18 acagttactt gatc 24
<210> <211> <212> <213>	22 DNA

```
<220>
                primer_bind
     <221>
                sense oligonucleotide primer based upon
     <223>
                intronic sequences of the PSMA genomic
                clone used to amplify the corresponding
                regions of the PSMA-like gene (exon 10)
     <400>
                19
                                                  22
tagatgctat tgagtcgttt gc
     <210>
                20
     <211>
                22
     <212>
               DNA
     <213>
               Artificial sequence
     <220>
     <221>
                primer_bind
                antisense oligonucleotide primer based upon
     <223>
                intronic sequences of the PSMA genomic
                clone used to amplify the corresponding
                regions of the PSMA-like gene (exon 10)
     <400>
                20
                                                  22
aaactgagac tcagataggc tg
     <210>
                21
     <211>
                22
     <212>
               DNA
     <213>
                Artificial sequence
     <220>
     <221>
               primer_bind
                sense oligonucleotide primer based upon
     <223>
                intronic sequences of the PSMA genomic
                clone used to amplify the corresponding
                regions of the PSMA-like gene (exon 11)
     <400>
                21
                                                  22
ctgggcttgg tagtgtcctg gg
     <210>
                22
     <211>
                24
     <212>
                DNA
     <213>
                Artificial sequence
     <220>
     <221>
                primer_bind
     <223>
                antisense oligonucleotide primer based upon
```

intronic sequences of the PSMA genomic clone used to amplify the corresponding regions of the PSMA-like gene (exon 11)

<400> gcttggcaaa	22 caagteetgg e	tac	24					
<210> <211> <212> <213>		al sequence						
<220> <221> <223>	sense ol intronic clone us	primer_bind sense oligonucleotide primer based upon intronic sequences of the PSMA genomic clone used to amplify the corresponding regions of the PSMA-like gene (exon 12)						
<400>	23							
tgtcgttaat	atgggtcagc t	C	22					
<210> <211> <212> <213> <220> <221> <223> <400> ttaactagac	DNA Artifici primer_h antisens intronic clone us	e oligonucleotide sequences of the ed to amplify the of the PSMA-like	corresponding					
<210> <211> <212> <213> <220> <221> <223>	25 22 DNA Artifici primer_b sense ol intronic clone us	al sequence	PSMA genomic corresponding					

22

<400>

tggtaggaat ttagcagtgg tc

caatcccaca ctgaattcag tg

25

22

```
<210>
               29
     <211>
               22
     <212>
               DNA
     <213>
               Artificial sequence
     <220>
     <221>
               primer bind
     <223>
               sense oligonucleotide primer based upon
               intronic sequences of the PSMA genomic
               clone used to amplify the corresponding
               regions of the PSMA-like gene (exon 15)
     <400>
               29
agaatggggt ttagtttaat gg
                                                22
     <210>
               30
     <211>
               21
     <212>
               DNA
     <213>
               Artificial sequence
     <220>
     <221>
               primer_bind
               antisense oligonucleotide primer based upon
     <223>
               intronic sequences of the PSMA genomic
               clone used to amplify the corresponding
               regions of the PSMA-like gene (exon 15)
     <400>
               30
                                                21
tgagtcactt tttggagtca g
     <210>
               31
     <211>
               22
     <212>
               DNA
     <213>
               Artificial sequence
     <220>
     <221>
               primer_bind
     <223>
               sense oligonucleotide primer based upon
               intronic sequences of the PSMA genomic
               clone used to amplify the corresponding
               regions of the PSMA-like gene (exons 16-17)
     <400>
               31
                                                22
ttgtaagcta tccctataag ag
               32
     <210>
     <211>
               22
     <212>
               DNA
               Artificial sequence
     <213>
```

```
<220>
     <221>
               primer_bind
               antisense oligonucleotide primer based upon
     <223>
                intronic sequences of the PSMA genomic
               clone used to amplify the corresponding
               regions of the PSMA-like gene (exons 16-17)
     <400>
                32
agttcagcaa cagtcatgtt ag
                                                22
     <210>
               33
     <211>
               22
     <212>
               DNA
     <213>
               Artificial sequence
     <220>
     <221>
               primer_bind
     <223>
               sense oligonucleotide primer based upon
               intronic sequences of the PSMA genomic
               clone used to amplify the corresponding
               regions of the PSMA-like gene (exon 18)
     <400>
               33
                                                22
gggtggtcct gaaaccaatc cc
     <210>
               34
               22
     <211>
     <212>
               DNA
     <213>
               Artificial sequence
     <220>
     <221>
               primer_bind
               antisense oligonucleotide primer based upon
     <223>
               intronic sequences of the PSMA genomic
               clone used to amplify the corresponding
               regions of the PSMA-like gene (exon 18)
               34
     <400>
                                                21
gtgatattac agaaaggagt c
     <210>
               35
     <211>
               22
     <212>
               DNA
     <213>
               Artificial sequence
     <220>
     <221>
               primer_bind
               sense oligonucleotide primer based upon
     <223>
```

intronic sequences of the PSMA genomic clone used to amplify the corresponding regions of the PSMA-like gene (exon 19)

		_	_					
	<400>	35						
	atccaggaat	tgcagagtgc tc		22				
	<210>	36						
	<211>							
	<212>							
	<213>		emience					
	\213>	ALCITICIAL SC	equence					
	<220>							
	<221>	primer_bind						
	<223>		mer based upon					
			intronic sequences of the PSMA genomic					
			clone used to amplify the corresponding					
			ne PSMA-like gene					
		10910112 01 01		(,				
	<400>	36						
mare.	ttcagtttta	atccataggg ag		22				
Fred.	J							
L								
U	<210>	37						
4	<211>							
Li	<212>							
LU	<213>		equence					
	\Z_13/	merreral sc	equence					
TU	<220>							
	<221>	primer_bind						
L	<223>	<u> </u>	(exon 10) used for	or performing				
			from various tiss					
		1011 011 021111						
₩# .#1	<400>	37						
*## ##		cattctggga ggtc		24				
	acagacacge	cacceggga ggce		24				
 - 4								
	<210>	38						
	<211>	24						
	<212>							
	<213>	Artificial se	equence					
	2000							
	<220>							
	<221>	<u> </u>		1 C				
	<223>		imer (exon 16) use					
			CR on cDNAs from v	arious				
		tissues						
	400	2.0						
	<400>	38		2.4				
	actgtgatac	agtggatagc cgct		24				